

SUBSTITUTE SEQUENCE LISTING

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<120> CHIMERIC PROTEIN FOR THE SCREENING OF AGONISTS AND ANTAGONISTS OF
 CELL SIGNALLING PATHWAYS THAT ARE DEPENDENT ON G-PROTEIN-COUPLED
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<140> 10/540,247
 <141> 2005-06-22

<150> PCT/FR03/003860
 <151> 2003-12-22

<150> FR 02/16576
 <151> 2002-12-23

<160> 14

<170> PatentIn version 3.3

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Ser	Ala	Asp	Ser	Tyr	Thr	Ser	Arg	Pro	Ser	Leu	Asp	Ser	Asp	Val	Ser	
			20					25					30			
ctg gag gag gac cgg gag agt gcc cgg cga gaa gtg gag agt cag gct																144

Leu	Glu	Glu	Asp	Arg	Glu	Ser	Ala	Arg	Arg	Glu	Val	Glu	Ser	Gln	Ala		
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cag	cag	cag	ctg	gaa	aga	gcc	aag	cac	aaa	cct	gtg	gca	ttt	gct	gtg	192	
Gln	Gln	Gln	Leu	Glu	Arg	Ala	Lys	His	Lys	Pro	Val	Ala	Phe	Ala	Val		
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Gln	Gly	Ser	Gly	Val	Asn	Phe	Glu	Ala	Lys	Asp	Phe	Leu	His	Ile	Lys		
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Gly	Asp	Ile	Ala	Phe	Ile	Pro	Ser	Pro	Gln	Arg	Leu	Glu	Ser	Ile	Arg		
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ctc	aaa	cag	gaa	cag	aag	gcc	agg	aga	tcc	ggg	aac	cct	tcc	agc	ctg	432	
Leu	Lys	Gln	Glu	Gln	Lys	Ala	Arg	Arg	Ser	Gly	Asn	Pro	Ser	Ser	Leu		
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agt	gac	att	ggc	aac	cga	cgt	tcc	cct	cct	cca	tct	cta	gcc	aag	cag	480	
Ser	Asp	Ile	Gly	Asn	Arg	Arg	Ser	Pro	Pro	Pro	Ser	Leu	Ala	Lys	Gln		
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Lys	Gln	Lys	Gln	Ala	Glu	His	Val	Pro	Pro	Tyr	Asp	Val	Val	Pro	Ser		
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Met	Arg	Pro	Val	Val	Leu	Val	Gly	Pro	Ser	Leu	Lys	Gly	Tyr	Glu	Val		
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aca	gac	atg	atg	cag	aag	gct	ctc	ttc	gac	ttc	ctt	aaa	cac	agg	ttt	624	
Thr	Asp	Met	Met	Gln	Lys	Ala	Leu	Phe	Asp	Phe	Leu	Lys	His	Arg	Phe		
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Asp	Gly	Arg	Ile	Ser	Ile	Thr	Arg	Val	Thr	Ala	Asp	Leu	Ser	Leu	Ala		
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Lys	Arg	Ser	Val	Leu	Asn	Asn	Pro	Gly	Lys	Arg	Thr	Ile	Ile	Glu	Arg		
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Ser	Ser	Ala	Arg	Ser	Ser	Ile	Ala	Glu	Val	Gln	Ser	Glu	Ile	Glu	Arg		
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ata	ttc	gag	ctg	gcc	aaa	tcc	ctg	cag	cta	gtg	gtg	ttg	gat	gct	gac	816	
Ile	Phe	Glu	Leu	Ala	Lys	Ser	Leu	Gln	Leu	Val	Val	Leu	Asp	Ala	Asp		

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Thr Ile Asn His Pro Ala Gln Leu Ala Lys Thr Ser Leu Ala Pro Ile			
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Ile Val Phe Val Lys Val Ser Ser Pro Lys Val Leu Gln Arg Leu Ile			
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Arg Ser Arg Gly Lys Ser Gln Met Lys His Leu Thr Val Gln Met Met			
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gca tat gat aag ctg gtt cag tgc cca cct gag tca ttt gat gtg att			1008
Ala Tyr Asp Lys Leu Val Gln Cys Pro Pro Glu Ser Phe Asp Val Ile			
325	330	335	
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Leu Asp Glu Asn Gln Leu Asp Asp Ala Cys Glu His Leu Ala Glu Tyr			
340	345	350	
cta gag gtt tac tgg cgc gct acc cac cac cca gca ccg ggc ccc ggg			1104
Leu Glu Val Tyr Trp Arg Ala Thr His His Pro Ala Pro Gly Pro Gly			
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Met Leu Gly Pro Pro Ser Ala Ile Pro Gly Leu Gln Asn Gln Gln Leu			
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Leu Gly Glu Arg Gly Glu Glu His Ser Pro Leu Glu Arg Asp Ser Leu			
385	390	395	400
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Met Pro Ser Asp Glu Ala Ser Glu Ser Ser Arg Gln Ala Trp Thr Gly			
405	410	415	
tct tca cag cgc agc tcc cgc cat ctg gag gag gac tat gca gat gcc			1296
Ser Ser Gln Arg Ser Ser Arg His Leu Glu Glu Asp Tyr Ala Asp Ala			
420	425	430	
tac cag gac ctg tac cag cct cac cgt caa cac acc tcg ggg cta ccc			1344
Tyr Gln Asp Leu Tyr Gln Pro His Arg Gln His Thr Ser Gly Leu Pro			
435	440	445	
agt gct aac ggg cat gac ccc caa gac cgg ctc cta gcc cag gac tcg			1392
Ser Ala Asn Gly His Asp Pro Gln Asp Arg Leu Leu Ala Gln Asp Ser			
450	455	460	
gag cat gac cac aat gac cgg aac tgg cag cgt aac cgg cct tgg cct			1440
Glu His Asp His Asn Asp Arg Asn Trp Gln Arg Asn Arg Pro Trp Pro			
465	470	475	480
aag gac agc tac gaa ttc gcc aaa gaa agg gag cgg gtg gag aac cgg			1488
Lys Asp Ser Tyr Glu Phe Ala Lys Glu Arg Glu Arg Val Glu Asn Arg			
485	490	495	

cgc gca ttc ctg aag ctg cgg cgg cag cag cag att gaa cgc gag ctc	1536
Arg Ala Phe Leu Lys Leu Arg Arg Gln Gln Gln Ile Glu Arg Glu Leu	
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aac ggg tac atg gag tgg atc tca aaa gca gaa gag gtg atc ctc gca	1584
Asn Gly Tyr Met Glu Trp Ile Ser Lys Ala Glu Glu Val Ile Leu Ala	
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gag gac gag acc gac gtg gag cag aga cat ccc ttt gat gga gct ctg	1632
Glu Asp Glu Thr Asp Val Glu Gln Arg His Pro Phe Asp Gly Ala Leu	
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cgg aga gcc act atc aag aag agc aag acg gac ctg ctc cac cca gag	1680
Arg Arg Ala Thr Ile Lys Lys Ser Lys Thr Asp Leu Leu His Pro Glu	
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Glu Ala Glu Asp Gln Leu Ala Asp Ile Ala Ser Val Gly Ser Pro Phe	
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gcc cga gcc agc att aaa agt gcc aag ctg gag aac tcg agt ttt ttc	1776
Ala Arg Ala Ser Ile Lys Ser Ala Lys Leu Glu Asn Ser Ser Phe Phe	
580 585 590	
cac aaa aaa gag agg aga atg cgt ttc tac atc cgt cgc atg gtc aaa	1824
His Lys Lys Glu Arg Arg Met Arg Phe Tyr Ile Arg Arg Met Val Lys	
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act cag taa	1833
Thr Gln	
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35 40 45	
Gln Gln Gln Leu Glu Arg Ala Lys His Lys Pro Val Ala Phe Ala Val	
50 55 60	

Arg Thr Asn Val Ser Tyr Cys Gly Val Leu Asp Glu Glu Cys Pro Val
 65 70 75 80

Gln Gly Ser Gly Val Asn Phe Glu Ala Lys Asp Phe Leu His Ile Lys
 85 90 95

Glu Lys Tyr Ser Asn Asp Trp Trp Ile Gly Arg Leu Val Lys Glu Gly
 100 105 110

Gly Asp Ile Ala Phe Ile Pro Ser Pro Gln Arg Leu Glu Ser Ile Arg
 115 120 125

Leu Lys Gln Glu Gln Lys Ala Arg Arg Ser Gly Asn Pro Ser Ser Leu
 130 135 140

Ser Asp Ile Gly Asn Arg Arg Ser Pro Pro Pro Ser Leu Ala Lys Gln
 145 150 155 160

Lys Gln Lys Gln Ala Glu His Val Pro Pro Tyr Asp Val Val Pro Ser
 165 170 175

Met Arg Pro Val Val Leu Val Gly Pro Ser Leu Lys Gly Tyr Glu Val
 180 185 190

Thr Asp Met Met Gln Lys Ala Leu Phe Asp Phe Leu Lys His Arg Phe
 195 200 205

Asp Gly Arg Ile Ser Ile Thr Arg Val Thr Ala Asp Leu Ser Leu Ala
 210 215 220

Lys Arg Ser Val Leu Asn Asn Pro Gly Lys Arg Thr Ile Ile Glu Arg
 225 230 235 240

Ser Ser Ala Arg Ser Ser Ile Ala Glu Val Gln Ser Glu Ile Glu Arg
 245 250 255

Ile Phe Glu Leu Ala Lys Ser Leu Gln Leu Val Val Leu Asp Ala Asp
 260 265 270

Thr Ile Asn His Pro Ala Gln Leu Ala Lys Thr Ser Leu Ala Pro Ile
 275 280 285

Ile Val Phe Val Lys Val Ser Ser Pro Lys Val Leu Gln Arg Leu Ile

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Ala Tyr Asp Lys Leu Val Gln Cys Pro Pro Glu Ser Phe Asp Val Ile				
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Leu Glu Val Tyr Trp Arg Ala Thr His His Pro Ala Pro Gly Pro Gly				
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Met Leu Gly Pro Pro Ser Ala Ile Pro Gly Leu Gln Asn Gln Gln Leu				
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Ser Ser Gln Arg Ser Ser Arg His Leu Glu Glu Asp Tyr Ala Asp Ala				
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Tyr Gln Asp Leu Tyr Gln Pro His Arg Gln His Thr Ser Gly Leu Pro				
	435		440	445
Ser Ala Asn Gly His Asp Pro Gln Asp Arg Leu Leu Ala Gln Asp Ser				
	450		455	460
Glu His Asp His Asn Asp Arg Asn Trp Gln Arg Asn Arg Pro Trp Pro				
465		470		475 480
Lys Asp Ser Tyr Glu Phe Ala Lys Glu Arg Glu Arg Val Glu Asn Arg				
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Arg Ala Phe Leu Lys Leu Arg Arg Gln Gln Gln Ile Glu Arg Glu Leu				
	500		505	510
Asn Gly Tyr Met Glu Trp Ile Ser Lys Ala Glu Glu Val Ile Leu Ala				
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Glu Asp Glu Thr Asp Val Glu Gln Arg His Pro Phe Asp Gly Ala Leu
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Arg Arg Ala Thr Ile Lys Lys Ser Lys Thr Asp Leu Leu His Pro Glu
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Glu Ala Glu Asp Gln Leu Ala Asp Ile Ala Ser Val Gly Ser Pro Phe
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Ala Arg Ala Ser Ile Lys Ser Ala Lys Leu Glu Asn Ser Ser Phe Phe
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His Lys Lys Glu Arg Arg Met Arg Phe Tyr Ile Arg Arg Met Val Lys
595 600 605

Thr Gln
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